

- 113
56. 57. 58. 59. 60. 61. 62. 63.
- (b) optionally, identifying amino acids in said (poly)peptide sequences to be modified so as to remove unfavorable interactions between amino acids within or between said or other (poly)peptide sequences;
 - (c) identifying at least one structural sub-element within each of said (poly)peptide sequences;
 - (d) backtranslating each of said (poly)peptide sequences into a corresponding coding nucleic acid sequence;
 - (e) setting up cleavage sites in regions adjacent to or between the ends of sub-sequences encoding said sub-elements, each of said cleavage sites:
 - (ea) being unique within each of said coding nucleic acid sequences;
 - (eb) being common to the corresponding sub-sequences of any said coding nucleic acids;

wherein said vector is essentially devoid of any of said cleavage sites.

57. A collection of vectors comprising a plurality of vectors according to claim

56.

58. A vector according to claim 56, wherein said vector is an expression vector.

59. A collection of vectors comprising a plurality of vectors according to claim

58.

60. A kit comprising a vector according to claim 56.

61. A kit comprising a collection of vectors according to claim 57.

62. A kit comprising a vector according to claim 58.

63. A kit comprising a collection of vectors according to claim 59.